



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/701,586
Source: O1PE
Date Processed by STIC: 6/5/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).

Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
<http://www.uspto.gov/web/offices/pac/checker>

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/701,586

DATE: 06/05/2001
TIME: 12:16:01

Input Set: A:\es.txt
Output Set: C:\CRF3\06052001\I701586.raw

3 <110> APPLICANT: Kock, Michael
 4 Hoeger, Thomas
 5 Kroeger, Burkhard
 6 Otterbach, Bernd
 7 Lubisch, Wilfried
 8 Lemaire, Hans-Georg
 10 <120> TITLE OF INVENTION: Poly (ADP-ribose) polymerase-gene
 12 <130> FILE REFERENCE: 0050/49100
 14 <140> CURRENT APPLICATION NUMBER: US 09/701,586
 15 <141> CURRENT FILING DATE: 2000-11-30
 17 <150> PRIOR APPLICATION NUMBER: PCT/EP99/03889
 18 <151> PRIOR FILING DATE: 1999-06-04
 20 <160> NUMBER OF SEQ ID NOS: 33
 22 <170> SOFTWARE: PatentIn/WordPerfect

Does Not Comply
Corrected Diskette Needed

*more
throughout*

OK

ERRORED SEQUENCES

148 <210> SEQ ID NO: 2
 149 <211> LENGTH: 571 S70 (see next page)
 150 <212> TYPE: PRT
 151 <213> ORGANISM: Homo sapiens
 153 <400> SEQUENCE: 2
 155 Met Ala Ala Arg Arg Arg Arg Ser Thr Gly Gly Gly Arg Ala Arg Ala
 156 1 5 10 15
 157 Leu Asn Glu Ser Lys Arg Val Asn Asn Gly Asn Thr Ala Pro Glu Asp
 158 20 25 30
 159 Ser Ser Pro Ala Lys Lys Thr Arg Arg Cys Gln Arg Gln Glu Ser Lys
 160 35 40 45
 161 Lys Met Pro Val Ala Gly Gly Lys Ala Asn Lys Asp Arg Thr Glu Asp
 162 50 55 60
 163 Lys Gln Asp Glu Ser Val Lys Ala Leu Leu Lys Gly Lys Ala Pro
 164 65 70 75 80
 165 Val Asp Pro Glu Cys Thr Ala Lys Val Gly Lys Ala His Val Tyr Cys
 166 85 90 95
 167 Glu Gly Asn Asp Val Tyr Asp Val Met Leu Asn Gln Thr Asn Leu Gln
 168 100 105 110
 169 Phe Asn Asn Asn Lys Tyr Tyr Leu Ile Gln Leu Leu Glu Asp Asp Ala
 170 115 120 125
 171 Gln Arg Asn Phe Ser Val Trp Met Arg Trp Gly Arg Val Gly Lys Met
 172 130 135 140
 173 Gly Gln His Ser Leu Val Ala Cys Ser Gly Asn Leu Asn Lys Ala Lys
 174 145 150 155 160
 175 Glu Ile Phe Gln Lys Lys Phe Leu Asp Lys Thr Lys Asn Asn Trp Glu
 176 165 170 175
 177 Asp Arg Glu Lys Phe Glu Lys Val Pro Gly Lys Tyr Asp Met Leu Gln
 178 180 185 190

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Input Set : A:\es.txt

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179 Met Asp Tyr Ala Thr Asn Thr Gln Asp Glu Glu Glu Thr Lys Lys Glu
 180 195 200 205
 181 Glu Ser Leu Lys Ser Pro Leu Lys Pro Glu Ser Gln Leu Asp Leu Arg
 182 210 215 220
 183 Val Gln Glu Leu Ile Lys Leu Ile Cys Asn Val Gln Ala Met Glu Glu
 184 225 230 235 240
 185 Met Met Met Glu Met Lys Tyr Asn Thr Lys Lys Ala Pro Leu Gly Lys
 186 245 250 255
 187 Leu Thr Val Ala Gln Ile Lys Ala Gly Tyr Gln Ser Leu Lys Lys Ile
 188 260 265 270
 189 Glu Asp Cys Ile Arg Ala Gly Gln His Gly Arg Ala Leu Met Glu Ala
 190 275 280 285
 191 Cys Asn Glu Phe Tyr Thr Arg Ile Pro His Asp Phe Gly Leu Arg Thr
 192 290 295 300
 193 Pro Pro Leu Ile Arg Thr Gln Lys Glu Leu Ser Glu Lys Ile Gln Leu
 194 305 310 315 320
 195 Leu Glu Ala Leu Gly Asp Ile Glu Ile Ala Ile Lys Leu Val Lys Thr
 196 325 330 335
 197 Glu Leu Gln Ser Pro Glu His Pro Leu Asp Gln His Tyr Arg Asn Leu
 198 340 345 350
 199 His Cys Ala Leu Arg Pro Leu Asp His Glu Ser Tyr Glu Phe Lys Val
 200 355 360 365
 201 Ile Ser Gln Tyr Leu Gln Ser Thr His Ala Pro Thr His Ser Asp Tyr
 202 370 375 380
 203 Thr Met Thr Leu Leu Asp Leu Phe Glu Val Glu Lys Asp Gly Glu Lys
 204 385 390 395 400
 205 Glu Ala Phe Arg Glu Asp Leu His Asn Arg Met Leu Leu Trp His Gly
 206 405 410 415
 207 Ser Arg Met Ser Asn Trp Val Gly Ile Leu Ser His Gly Leu Arg Ile
 208 420 425 430
 209 Ala Pro Pro Glu Ala Pro Ile Thr Gly Tyr Met Phe Gly Lys Gly Ile
 210 435 440 445
 211 Tyr Phe Ala Asp Met Ser Ser Lys Ser Ala Asn Tyr Cys Phe Ala Ser
 212 450 455 460
 213 Arg Leu Lys Asn Thr Gly Leu Leu Leu Ser Glu Val Ala Leu Gly
 214 465 470 475 480
 215 Gln Cys Asn Glu Leu Leu Glu Ala Asn Pro Lys Ala Glu Gly Leu Leu
 216 485 490 495
 217 Gln Gly Lys His Ser Thr Lys Gly Leu Gly Lys Met Ala Pro Ser Ser
 218 500 505 510
 219 Ala His Phe Val Thr Leu Asn Gly Ser Thr Val Pro Leu Gly Pro Ala
 220 515 520 525
 221 Ser Asp Thr Gly Ile Leu Asn Pro Asp Gly Tyr Thr Leu Asn Tyr Asn
 222 530 535 540
 223 Glu Tyr Ile Val Tyr Asn Pro Asn Gln Val Arg Met Arg Tyr Leu Leu
 224 545 550 555 560
 E--> 225 Lys Val Gln Phe Asn Phe Leu Gln Leu Trp * *O delete stop codon*
 226 565 570
 356 <210> SEQ ID NO: 4

RAW SEQUENCE LISTING
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Input Set : A:\es.txt
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357 <211> LENGTH: 533 (next page)
 358 <212> TYPE: PRT
 359 <213> ORGANISM: Homo sapiens
 361 <400> SEQUENCE: 4
 363 Met Ala Pro Lys Pro Lys Pro Trp Val Gln Thr Glu Gly Pro Glu Lys
 364 1 5 10 15
 365 Lys Lys Gly Arg Gln Ala Gly Arg Glu Glu Asp Pro Phe Arg Ser Thr
 366 20 25 30
 367 Ala Glu Ala Leu Lys Ala Ile Pro Ala Glu Lys Arg Ile Ile Arg Val
 368 35 40 45
 369 Asp Pro Thr Cys Pro Leu Ser Ser Asn Pro Gly Thr Gln Val Tyr Glu
 370 50 55 60
 371 Asp Tyr Asn Cys Thr Leu Asn Gln Thr Asn Ile Glu Asn Asn Asn Asn
 372 65 70 75 80
 373 Lys Phe Tyr Ile Ile Gln Leu Leu Gln Asp Ser Asn Arg Phe Phe Thr
 374 85 90 95
 375 Cys Trp Asn Arg Trp Gly Arg Val Gly Glu Val Gly Gln Ser Lys Ile
 376 100 105 110
 377 Asn His Phe Thr Arg Leu Glu Asp Ala Lys Lys Asp Phe Glu Lys Lys
 378 115 120 125
 379 Phe Arg Glu Lys Thr Lys Asn Asn Trp Ala Glu Arg Asp His Phe Val
 380 130 135 140
 381 Ser His Pro Gly Lys Tyr Thr Leu Ile Glu Val Gln Ala Glu Asp Glu
 382 145 150 155 160
 383 Ala Gln Glu Ala Val Val Lys Val Asp Arg Gly Pro Val Arg Thr Val
 384 165 170 175
 385 Thr Lys Arg Val Gln Pro Cys Ser Leu Asp Pro Ala Thr Gln Lys Leu
 386 180 185 190
 387 Ile Thr Asn Ile Phe Ser Lys Glu Met Phe Lys Asn Thr Met Ala Leu
 388 195 200 205
 389 Met Asp Leu Asp Val Lys Lys Met Pro Leu Gly Lys Leu Ser Lys Gln
 390 210 215 220
 391 Gln Ile Ala Arg Gly Phe Glu Ala Leu Glu Ala Leu Glu Glu Ala Leu
 392 225 230 235 240
 393 Lys Gly Pro Thr Asp Gly Gly Gln Ser Leu Glu Glu Leu Ser Ser His
 394 245 250 255
 395 Phe Tyr Thr Val Ile Pro His Asn Phe Gly His Ser Gln Pro Pro Pro
 396 260 265 270
 397 Ile Asn Ser Pro Glu Leu Leu Gln Ala Lys Lys Asp Met Leu Leu Val
 398 275 280 285
 399 Leu Ala Asp Ile Glu Leu Ala Gln Ala Leu Gln Ala Val Ser Glu Gln
 400 290 295 300
 401 Glu Lys Thr Val Glu Glu Val Pro His Pro Leu Asp Arg Asp Tyr Gln
 402 305 310 315 320
 403 Leu Leu Lys Cys Gln Leu Gln Leu Leu Asp Ser Gly Ala Pro Glu Tyr
 404 325 330 335
 405 Lys Val Ile Gln Thr Tyr Leu Glu Gln Thr Gly Ser Asn His Arg Cys
 406 340 345 350
 407 Pro Thr Leu Gln His Ile Trp Lys Val Asn Gln Glu Gly Glu Glu Asp

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408	355	360	365
409	Arg Phe Gln Ala His Ser Lys Leu Gly Asn Arg Lys Leu Leu Trp His		
410	370	375	380
411	Gly Thr Asn Met Ala Val Val Ala Ala Ile Leu Thr Ser Gly Leu Arg		
412	385	390	395
413	Ile Met Pro His Ser Gly Gly Arg Val Gly Lys Gly Ile Tyr Phe Ala		400
414	405	410	415
415	Ser Glu Asn Ser Lys Ser Ala Gly Tyr Val Ile Gly Met Lys Cys Gly		
416	420	425	430
417	Ala His His Val Gly Tyr Met Phe Leu Gly Glu Val Ala Leu Gly Arg		
418	435	440	445
419	Glu His His Ile Asn Thr Asp Asn Pro Ser Leu Lys Ser Pro Pro Pro		
420	450	455	460
421	Gly Phe Asp Ser Val Ile Ala Arg Gly His Thr Glu Pro Asp Pro Thr		
422	465	470	475
423	Gln Asp Thr Glu Leu Glu Leu Asp Gly Gln Gln Val Val Val Pro Gln		480
424	485	490	495
425	Gly Gln Pro Val Pro Cys Pro Glu Phe Ser Ser Ser Thr Phe Ser Gln		
426	500	505	510
427	Ser Glu Tyr Leu Ile Tyr Gln Glu Ser Gln Cys Arg Leu Arg Tyr Leu		
428	515	520	525
E-->	429 Leu Glu Val His Leu	*	delete
430	530		
561	<210> SEQ ID NO: 6		
562	<211> LENGTH: 541	540	(next page)
563	<212> TYPE: PRT		
564	<213> ORGANISM: Homo sapiens		
566	<400> SEQUENCE: 6		
568	Met Ser Leu Leu Phe Leu Ala Met Ala Pro Lys Pro Lys Pro Trp Val		
569	1	5	10
570	5	10	15
571	Gln Thr Glu Gly Pro Glu Lys Lys Gly Arg Gln Ala Gly Arg Glu		
572	20	25	30
573	Glu Asp Pro Phe Arg Ser Thr Ala Glu Ala Leu Lys Ala Ile Pro Ala		
574	35	40	45
575	Glu Lys Arg Ile Ile Arg Val Asp Pro Thr Cys Pro Leu Ser Ser Asn		
576	50	55	60
577	Pro Gly Thr Gln Val Tyr Glu Asp Tyr Asn Cys Thr Leu Asn Gln Thr		
578	65	70	75
579	75	80	80
580	Asn Ile Glu Asn Asn Asn Lys Phe Tyr Ile Ile Gln Leu Leu Gln		
581	85	90	95
582	Asp Ser Asn Arg Phe Phe Thr Cys Trp Asn Arg Trp Gly Arg Val Gly		
583	100	105	110
584	Glu Val Gly Gln Ser Lys Ile Asn His Phe Thr Arg Leu Glu Asp Ala		
585	115	120	125
586	Lys Lys Asp Phe Glu Lys Lys Phe Arg Glu Lys Thr Lys Asn Asn Trp		
587	130	135	140
588	Ala Glu Arg Asp His Phe Val Ser His Pro Gly Lys Tyr Thr Leu Ile		
589	145	150	155
590	155	160	
591	Glu Val Gln Ala Glu Asp Glu Ala Gln Glu Ala Val Val Lys Val Asp		

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589	165	170	175
590	Arg Gly Pro Val Arg Thr Val Thr Lys Arg Val Gln Pro Cys Ser Leu		
591	180	185	190
592	Asp Pro Ala Thr Gln Lys Leu Ile Thr Asn Ile Phe Ser Lys Glu Met		
593	195	200	205
594	Phe Lys Asn Thr Met Ala Leu Met Asp Leu Asp Val Lys Lys Met Pro		
595	210	215	220
596	Leu Gly Lys Leu Ser Lys Gln Gln Ile Ala Arg Gly Phe Glu Ala Leu		
597	225	230	235
598	Glu Ala Leu Glu Glu Ala Leu Lys Gly Pro Thr Asp Gly Gly Gln Ser		
599	245	250	255
600	Leu Glu Glu Leu Ser Ser His Phe Tyr Thr Val Ile Pro His Asn Phe		
601	260	265	270
602	Gly His Ser Gln Pro Pro Pro Ile Asn Ser Pro Glu Leu Leu Gln Ala		
603	275	280	285
604	Lys Lys Asp Met Leu Leu Val Leu Ala Asp Ile Glu Leu Ala Gln Ala		
605	290	295	300
606	Leu Gln Ala Val Ser Glu Gln Glu Lys Thr Val Glu Glu Val Pro His		
607	305	310	315
608	Pro Leu Asp Arg Asp Tyr Gln Leu Leu Lys Cys Gln Leu Gln Leu Leu		
609	325	330	335
610	Asp Ser Gly Ala Pro Glu Tyr Lys Val Ile Gln Thr Tyr Leu Glu Gln		
611	340	345	350
612	Thr Gly Ser Asn His Arg Cys Pro Thr Leu Gln His Ile Trp Lys Val		
613	355	360	365
614	Asn Gln Glu Gly Glu Asp Arg Phe Gln Ala His Ser Lys Leu Gly		
615	370	375	380
616	Asn Arg Lys Leu Leu Trp His Gly Thr Asn Met Ala Val Val Ala Ala		
617	385	390	395
618	Ile Leu Thr Ser Gly Leu Arg Ile Met Pro His Ser Gly Gly Arg Val		
619	405	410	415
620	Gly Lys Gly Ile Tyr Phe Ala Ser Glu Asn Ser Lys Ser Ala Gly Tyr		
621	420	425	430
622	Val Ile Gly Met Lys Cys Gly Ala His His Val Gly Tyr Met Phe Leu		
623	435	440	445
624	Gly Glu Val Ala Leu Gly Arg Glu His His Ile Asn Thr Asp Asn Pro		
625	450	455	460
626	Ser Leu Lys Ser Pro Pro Pro Gly Phe Asp Ser Val Ile Ala Arg Gly		
627	465	470	475
628	His Thr Glu Pro Asp Pro Thr Gln Asp Thr Glu Leu Glu Leu Asp Gly		
629	485	490	495
630	Gln Gln Val Val Val Pro Gln Gly Gln Pro Val Pro Cys Pro Glu Phe		
631	500	505	510
632	Ser Ser Ser Thr Phe Ser Gln Ser Glu Tyr Leu Ile Tyr Gln Glu Ser		
633	515	520	525
E--> 634	Gln Cys Arg Leu Arg Tyr Leu Leu Glu Val His Leu	*	delete
635	530	535	540

638 <210> SEQ ID NO: 7
639 <211> LENGTH: 1740

1739 (see pp. 6-8)

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TIME: 12:16:01

Input Set : A:\es.txt
Output Set: C:\CRF3\06052001\I701586.raw

640 <212> TYPE: DNA
 641 <213> ORGANISM: Mus musculus
 643 <220> FEATURE:
 644 <221> NAME/KEY: CDS
 645 <222> LOCATION: 112..1710
 647 <400> SEQUENCE: 7

E--> 649 ccggcttcc acttttctg ctgcctcgaa gacacacctcg agcacaactcg ttccctaaactcg
 E--> 650 agggtgggcgaa actgacgg gatctaagct tctgcatactc tgaggagaac c atg gct,
 651 Met Ala

E--> 653 cca aaa cga aag gcc tct gtg cag act gag ggc tcc aag aag cag cga
 654 Pro Lys Arg Lys Ala Ser Val Gln Thr Glu Gly Ser Lys Lys Gln Arg

W--> 655 545 550 555

E--> 656 caa ggg aca gag gag gag gac agc ttc cgg tcc act gcc gag gct ctc
 657 Gln Gly Thr Glu Glu Asp Ser Phe Arg Ser Thr Ala Glu Ala Leu

W--> 658 560 565 570 575

E--> 659 aga gca gca cct gct gat aat cgg gtc atc cgt gtg gac ccc tca tgt
 660 Arg Ala Ala Pro Ala Asp Asn Arg Val Ile Arg Val Asp Pro Ser Cys

W--> 661 580 585 590

E--> 662 cca ttc agc cgg aac ccc ggg ata cag gtc cac gag gac tat gac tgt
 663 Pro Phe Ser Arg Asn Pro Gly Ile Gln Val His Glu Asp Tyr Asp Cys

W--> 664 595 600 605

E--> 665 acc ctg aac cag acc aac atc ggc aac aac aac aag ttc tat att
 666 Thr Leu Asn Gln Thr Asn Ile Gly Asn Asn Asn Lys Phe Tyr Ile

W--> 667 610 615 620

E--> 668 atc caa ctg ctg gag gag ggt agt cgc ttc ttc tgc tgg aat cgc tgg
 669 Ile Gln Leu Leu Glu Glu Ser Arg Phe Phe Cys Trp Asn Arg Trp

W--> 670 625 630 635

E--> 671 ggc cgc gtg gga gag gtg ggc cag agc aag atg aac cac ttc acc tgc
 672 Gly Arg Val Gly Glu Val Gly Gln Ser Lys Met Asn His Phe Thr Cys

W--> 673 640 645 650 655

E--> 674 ctg gaa gat gca aag aag gac ttt aag aag aaa ttt tgg gag aag act
 675 Leu Glu Asp Ala Lys Lys Asp Phe Lys Lys Phe Trp Glu Lys Thr

W--> 676 660 665 670

E--> 677 aaa aac aaa tgg gag gag cgg gac cgt ttt gtg gcc cag ccc aac aag
 678 Lys Asn Lys Trp Glu Glu Arg Asp Arg Phe Val Ala Gln Pro Asn Lys

W--> 679 675 680 685

E--> 680 tac aca ctt ata gaa gtc cag gga gaa gca gag agc caa gag gct gta
 681 Tyr Thr Leu Ile Glu Val Gln Gly Glu Ala Glu Ser Gln Glu Ala Val

W--> 682 690 695 700

E--> 683 gtg aag gcc tta tct ccc cag gtg gac agc ggc cct gtg agg acc gtg
 684 Val Lys Ala Leu Ser Pro Gln Val Asp Ser Gly Pro Val Arg Thr Val

W--> 685 705 710 715

E--> 686 gtc aag ccc tgc tcc cta gac cct gcc acc cag aac ctt atc acc aac
 687 Val Lys Pro Cys Ser Leu Asp Pro Ala Thr Gln Asn Leu Ile Thr Asn

W--> 688 720 725 730 735

E--> 689 atc ttc agc aaa gag atg ttc aag aac gca atg acc ctc atg aac ctg
 690 Ile Phe Ser Lys Glu Met Phe Lys Asn Ala Met Thr Leu Met Asn Leu

W--> 691 740 745 750

E--> 692 gat gtg aag aag atg ccc ttg gga aag ctg acc aag cag cag att gcc 789

60 59
117
165 numbers
213 off



309

357

405

453

501

549

597

645

693

741

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Input Set : A:\es.txt
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693	Asp	Val	Lys	Lys	Met	Pro	Leu	Gly	Lys	Leu	Thr	Lys	Gln	Gln	Ile	Ala	
W--> 694			755				760			765							nos. off
E--> 695	cgt	ggc	tcc	gag	gcc	ttg	gaa	gct	cta	gag	gag	gcc	atg	aaa	aac	ccc	837
696	Arg	Gly	Phe	Glu	Ala	Leu	Glu	Ala	Leu	Glu	Glu	Ala	Met	Lys	Asn	Pro	
W--> 697			770				775			780							
E--> 698	aca	ggg	gat	ggc	cag	agc	ctg	gaa	gag	ctc	tcc	tcc	tgc	ttc	tac	act	885
699	Thr	Gly	Asp	Gly	Gln	Ser	Leu	Glu	Glu	Leu	Ser	Ser	Cys	Phe	Tyr	Thr	
W--> 700			785				790			795							
E--> 701	gtc	atc	cca	cac	aac	tcc	ggc	cgc	agc	cga	ccc	ccc	atc	aac	tcc		933
702	Val	Ile	Pro	His	Asn	Phe	Gly	Arg	Ser	Arg	Pro	Pro	Pro	Ile	Asn	Ser	
W--> 703	800				805					810				815			
E--> 704	cct	gat	gtg	ctt	cag	gcc	aag	aag	gac	atg	ctg	ctg	gtg	cta	gcg	gac	981
705	Pro	Asp	Val	Leu	Gln	Ala	Lys	Lys	Asp	Met	Leu	Leu	Val	Leu	Ala	Asp	
W--> 706			820				825			830							
E--> 707	atc	gag	ttg	gcg	cag	acc	ttg	cag	gca	gcc	cct	ggg	gag	gag	gag	gag	1029
708	Ile	Glu	Leu	Ala	Gln	Thr	Leu	Gln	Ala	Ala	Pro	Gly	Glu	Glu	Glu		
W--> 709			835				840			845							
E--> 710	aaa	gtg	gaa	gag	gtg	cca	cac	cca	ctg	gat	cga	gac	tac	cag	ctc	ctc	1077
711	Lys	Val	Glu	Glu	Val	Pro	His	Pro	Leu	Asp	Arg	Asp	Tyr	Gln	Leu	Leu	
W--> 712			850				855			860							
E--> 713	agg	tgc	cag	ctt	caa	ctg	ctg	gac	tcc	ggg	gag	tcc	gag	tac	aag	gca	1125
714	Arg	Cys	Gln	Leu	Gln	Leu	Leu	Asp	Ser	Gly	Glu	Ser	Glu	Tyr	Lys	Ala	
W--> 715			865				870			875							
E--> 716	ata	cag	acc	tac	ctg	aaa	cag	act	ggc	aac	agc	tac	agg	tgc	cca	aac	1173
717	Ile	Gln	Thr	Tyr	Leu	Lys	Gln	Thr	Gly	Asn	Ser	Tyr	Arg	Cys	Pro	Asn	
W--> 718	880				885				890			895					
E--> 719	ctg	cgg	cat	gtt	tgg	aaa	gtg	aac	cga	gaa	ggg	gag	gga	gac	agg	ttc	1221
720	Leu	Arg	His	Val	Trp	Lys	Val	Asn	Arg	Glu	Gly	Glu	Gly	Asp	Arg	Phe	
W--> 721			900				905			910							
E--> 722	cag	gcc	cac	tcc	aaa	ctg	ggc	aat	cgg	agg	ctg	ctg	tgg	cac	ggc	acc	1269
723	Gln	Ala	His	Ser	Lys	Leu	Gly	Asn	Arg	Arg	Leu	Leu	Trp	His	Gly	Thr	
W--> 724			915				920			925							
E--> 725	aat	gtg	gcc	gtg	gtg	gct	gcc	atc	ctc	acc	agt	ggg	ctc	cga	atc	atg	1317
726	Asn	Val	Ala	Val	Ala	Ala	Ile	Leu	Thr	Ser	Gly	Leu	Arg	Ile	Met		
W--> 727			930				935			940							
E--> 728	cca	cac	tcg	ggt	ggt	cgt	gtt	ggc	aag	ggt	att	tat	ttt	gcc	tct	gag	1365
729	Pro	His	Ser	Gly	Gly	Arg	Val	Gly	Lys	Gly	Ile	Tyr	Phe	Ala	Ser	Glu	
W--> 730			945				950			955							
E--> 731	aac	agc	aag	tca	gct	ggc	tat	gtt	acc	acc	atg	cac	tgt	ggg	ggc	cac	1413
732	Asn	Ser	Lys	Ser	Ala	Gly	Tyr	Val	Thr	Thr	Met	His	Cys	Gly	Gly	His	
W--> 733	960				965				970			975					
E--> 734	cag	gtg	ggc	tac	atg	tcc	ctg	ggc	gag	gtg	gcc	ctc	ggc	aaa	gag	cac	1461
735	Gln	Val	Gly	Tyr	Met	Phe	Leu	Gly	Glu	Val	Ala	Leu	Gly	Lys	Glu	His	
W--> 736			980				985			990							
E--> 737	cac	atc	acc	atc	gat	gac	ccc	agc	ttg	aag	agt	cca	ccc	cct	ggc	ttt	1509
738	His	Ile	Thr	Ile	Asp	Asp	Pro	Ser	Leu	Lys	Ser	Pro	Pro	Pro	Gly	Phe	
W--> 739			995				1000			1005							
E--> 740	gac	agc	gtc	atc	gcc	cga	ggc	caa	acc	gag	ccg	gat	ccc	gcc	cag	gac	1557
741	Asp	Ser	Val	Ile	Ala	Arg	Gly	Gln	Thr	Glu	Pro	Asp	Pro	Ala	Gln	Asp	

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W--> 742	1010	1015	1020	
E--> 743	att gaa ctt gaa ctg gat ggg cag ccg gtg gtg ccc caa ggc ccg			1605 nos.
744	Ile Glu Leu Glu Leu Asp Gly Gln Pro Val Val Val Pro Gln Gly Pro			
W--> 745	1025	1030	1035	off
E--> 746	cct gtg cag tgc ccg tca ttc aaa agc tcc agc ttc agc cag agt gaa			1653
747	Pro Val Gln Cys Pro Ser Phe Lys Ser Ser Phe Ser Gln Ser Glu			
W--> 748	1040	1045	1050	1055
E--> 749	tac ctc ata tac aag gag agc cag tgt cgc ctg cgc tac ctg ctg gag			1701
750	Tyr Leu Ile Tyr Lys Glu Ser Gln Cys Arg Leu Arg Tyr Leu Leu Glu			
W--> 751	1060	1065	1070	
E--> 752	att cac ctc taagctgctt gccctcccta ggtccaagcc			1740
E--> 753	Ile His Leu			
944	<210> SEQ ID NO: 10			
945	<211> LENGTH: 528			
946	<212> TYPE: DNA PRT			
947	<213> ORGANISM: Mus musculus			
949	<400> SEQUENCE: 10			
951	Met Ala Pro Lys Arg Lys Ala Ser Val Gln Thr Glu Gly Ser Lys Lys			
952	1 5 10 15			
953	Gln Arg Gln Gly Thr Glu Glu Asp Ser Phe Arg Ser Thr Ala Glu			
954	20 25 30			
955	Ala Leu Arg Ala Ala Pro Ala Asp Asn Arg Val Ile Arg Val Asp Pro			
956	35 40 45			
957	Ser Cys Pro Phe Ser Arg Asn Pro Gly Ile Gln Val His Glu Asp Tyr			
958	50 55 60			
959	Asp Cys Thr Leu Asn Gln Thr Asn Ile Gly Asn Asn Asn Lys Phe			
960	65 70 75 80			
961	Tyr Ile Ile Gln Leu Leu Glu Glu Gly Ser Arg Phe Phe Cys Trp Asn			
962	85 90 95			
963	Arg Trp Gly Arg Val Gly Glu Val Gly Gln Ser Lys Met Asn His Phe			
964	100 105 110			
965	Thr Cys Leu Glu Asp Ala Lys Lys Asp Phe Lys Lys Phe Trp Glu			
966	115 120 125			
967	Lys Thr Lys Asn Lys Trp Glu Glu Arg Asp Arg Phe Val Ala Gln Pro			
968	130 135 140			
969	Asn Lys Tyr Thr Leu Ile Glu Val Gln Gly Glu Ala Glu Ser Gln Glu			
970	145 150 155 160			
971	Ala Val Val Lys Val Asp Ser Gly Pro Val Arg Thr Val Val Lys Pro			
972	165 170 175			
973	Cys Ser Leu Asp Pro Ala Thr Gln Asn Leu Ile Thr Asn Ile Phe Ser			
974	180 185 190			
975	Lys Glu Met Phe Lys Asn Ala Met Thr Leu Met Asn Leu Asp Val Lys			
976	195 200 205			
977	Lys Met Pro Leu Gly Lys Leu Thr Lys Gln Gln Ile Ala Arg Gly Phe			
978	210 215 220			
979	Glu Ala Leu Glu Ala Leu Glu Glu Ala Met Lys Asn Pro Thr Gly Asp			
980	225 230 235 240			
981	Gly Gln Ser Leu Glu Leu Ser Ser Cys Phe Tyr Thr Val Ile Pro			
982	245 250 255			

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Input Set : A:\es.txt
Output Set: C:\CRF3\06052001\I701586.raw

983 His Asn Phe Gly Arg Ser Arg Pro Pro Pro Ile Asn Ser Pro Asp Val
 984 260 265 270
 985 Leu Gln Ala Lys Lys Asp Met Leu Leu Val Leu Ala Asp Ile Glu Leu
 986 275 280 285
 987 Ala Gln Thr Leu Gln Ala Ala Pro Gly Glu Glu Glu Lys Val Glu
 988 290 295 300
 989 Glu Val Pro His Pro Leu Asp Arg Asp Tyr Gln Leu Leu Arg Cys Gln
 990 305 310 315 320
 991 Leu Gln Leu Leu Asp Ser Gly Glu Ser Glu Tyr Lys Ala Ile Gln Thr
 992 325 330 335
 993 Tyr Leu Lys Gln Thr Gly Asn Ser Tyr Arg Cys Pro Asn Leu Arg His
 994 340 345 350
 995 Val Trp Lys Val Asn Arg Glu Gly Glu Gly Asp Arg Phe Gln Ala His
 996 355 360 365
 997 Ser Lys Leu Gly Asn Arg Arg Leu Leu Trp His Gly Thr Asn Val Ala
 998 370 375 380
 999 Val Val Ala Ala Ile Leu Thr Ser Gly Leu Arg Ile Met Pro His Ser
 1000 385 390 395 400
 1001 Gly Gly Arg Val Gly Lys Gly Ile Tyr Phe Ala Ser Glu Asn Ser Lys
 1002 405 410 415
 1003 Ser Ala Gly Tyr Val Thr Thr Met His Cys Gly Gly His Gln Val Gly
 1004 420 425 430
 1005 Tyr Met Phe Leu Gly Glu Val Ala Leu Gly Lys Glu His His Ile Thr
 1006 435 440 445
 1007 Ile Asp Asp Pro Ser Leu Lys Ser Pro Pro Pro Gly Phe Asp Ser Val
 1008 450 455 460
 1009 Ile Ala Arg Gly Gln Thr Glu Pro Asp Pro Ala Gln Asp Ile Glu Leu
 1010 465 470 475 480
 1011 Glu Leu Asp Gly Gln Pro Val Val Val Pro Gln Gly Pro Pro Val Gln
 1012 485 490 495
 1013 Cys Pro Ser Phe Lys Ser Ser Ser Phe Ser Gln Ser Glu Tyr Leu Ile
 1014 500 505 510
 1015 Tyr Lys Glu Ser Gln Cys Arg Leu Arg Tyr Leu Leu Glu Ile His Leu
 E--> 1016 515 520 525
 1241 <210> SEQ ID NO: 19
 1242 <211> LENGTH: 17
 1243 <212> TYPE: PRT
 1244 <213> ORGANISM: artificial sequence
 1246 <220> FEATURE:
 1247 <223> OTHER INFORMATION: part-sequence motif 5
 1249 <220> FEATURE:
 1250 <221> NAME/KEY: VARIANT
 1251 <222> LOCATION: 2..4, 6..7, 9, 13, 15..16
 1252 <223> OTHER INFORMATION: amino acid residues 2 to 4, 6 to 7, 9, 13 and 15 to 16 may
 be any
 1253 amino
 1254 acid
 E--> 1256 <400> 19 ← insert
 1258 Lys Xaa Xaa Xaa Leu Xaa Xaa Asp Ile Glu Xaa Ala Xaa Xaa
 1259 5 10 15

RAW SEQUENCE LISTING
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Input Set : A:\es.txt
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1261 Leu
 1264 <210> SEQ ID NO: 20
 1265 <211> LENGTH: 11
 1266 <212> TYPE: PRT
 1267 <213> ORGANISM: artificial sequence
E--> 1269 <200> invalid use <220>, instead
 1270 <223> OTHER INFORMATION: part-sequence motif 6
WK-> 1272 <220> FEATURE:
 1273 <221> NAME/KEY: VARIANT
 1274 <222> LOCATION: 2..4, 6
 1275 <223> OTHER INFORMATION: amino acid residues 2 to 4 and 6 may be any amino acid
 1277 <400> SEQUENCE: 20
WK 1279 Gly Xaa Xaa Xaa Leu Xaa Glu Val Ala Leu Gly
 1280 5 10
 1461 <210> SEQ ID NO: 31
 1462 <211> LENGTH: 10
 1463 <212> TYPE: PRT
 1464 <213> ORGANISM: Arabidopsis thaliana
E--> 1466
 1468 Ala Ala Val Leu Asp Gln Trp Ile Pro Asp
 1469 5 10
 1471 <210> SEQ ID NO: 32
 1472 <211> LENGTH: 39
 1473 <212> TYPE: DNA
 1474 <213> ORGANISM: Homo sapiens
 1476 <220> FEATURE:
 1477 <221> NAME/KEY: CDS
 1478 <222> LOCATION: 1..39
E--> 1480
 1482 gta tgc cag gaa ggt cat ggg cca gca aaa ggg tct ctg 39
 1483 Gly Met Pro Gly Arg Ser Trp Ala Ser Lys Arg Val Ser
 1484 5 10
 1487 <210> SEQ ID NO: 33
 1488 <211> LENGTH: 13
 1489 <212> TYPE: PRT
 1490 <213> ORGANISM: Homo sapiens
E--> 1492
 1494 Gly Met Pro Gly Arg Ser Trp Ala Ser Lys Arg Val Ser
 1495 5 10

see following pages for explanation

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<210> 29
<211> 7
<212> PRT
<213> artificial sequence

<220>
<223> NAD+ binding domain

<220>
<221> VARIANT
<222> 2..4
<223> amino acid residues 2 to 4 may be any amino acid residue
~~<400> 29~~ ~~29~~ Insert
Gly Xaa Xaa Xaa Gly Lys Gly
5

<210> 30
<211> 38
<212> PRT
<213> Artificial Sequence

<220>
<223> PARP zinc finger sequence motif

<220>
<221> VARIANT
<222> 2..3, 5..34, 36..37
<223> amino acid residues 2 to 3, 5 to 34 and 36 to 37 may be any amino acid residue; residues 33 and 34 may be present or absent
~~<400> 30~~ ~~30~~ insert
Cys Xaa Xaa Cys Xaa
5 10 15

Xaa
20 25 30

Xaa Xaa His Xaa Xaa Cys
35

<210> 31
<211> 10
<212> PRT
<213> Arabidopsis thaliana
~~<400> 31~~ <insert

Ala Ala Val Leu Asp Gln Trp Ile Pro Asp
5 10

<210> 32
<211> 39
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 1..39

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<400> 32 ← insert

gta tgc cag gaa ggt cat ggg cca gca aaa ggg tct ctg
Gly Met Pro Gly Arg Ser Trp Ala Ser Lys Arg Val Ser
5 10

39

<210> 33
<211> 13
<212> PRT
<213> Homo sapiens

<400> 33 ← insert

Gly Met Pro Gly Arg Ser Trp Ala Ser Lys Arg Val Ser
5 10

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Input Set : A:\es.txt
Output Set: C:\CRF3\06052001\I701586.raw

L:225 M:342 E: Invalid Stop Code On Error, STOP CODON:
L:241 M:112 C: (48) String data converted to lower case,
L:242 M:112 C: (48) String data converted to lower case,
L:243 M:112 C: (48) String data converted to lower case,
L:244 M:112 C: (48) String data converted to lower case,
L:245 M:112 C: (48) String data converted to lower case,
L:247 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:248 M:112 C: (48) String data converted to lower case,
L:250 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:251 M:112 C: (48) String data converted to lower case,
L:253 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:254 M:112 C: (48) String data converted to lower case,
L:256 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:257 M:112 C: (48) String data converted to lower case,
L:259 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:260 M:112 C: (48) String data converted to lower case,
L:262 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:263 M:112 C: (48) String data converted to lower case,
L:265 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:266 M:112 C: (48) String data converted to lower case,
L:268 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:269 M:112 C: (48) String data converted to lower case,
L:271 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:272 M:112 C: (48) String data converted to lower case,
L:274 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:275 M:112 C: (48) String data converted to lower case,
L:277 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:278 M:112 C: (48) String data converted to lower case,
L:280 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:281 M:112 C: (48) String data converted to lower case,
L:283 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:284 M:112 C: (48) String data converted to lower case,
L:286 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:287 M:112 C: (48) String data converted to lower case,
L:289 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:290 M:112 C: (48) String data converted to lower case,
L:292 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:293 M:112 C: (48) String data converted to lower case,
L:295 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:296 M:112 C: (48) String data converted to lower case,
L:298 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:299 M:112 C: (48) String data converted to lower case,
L:301 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:302 M:112 C: (48) String data converted to lower case,
L:304 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:305 M:112 C: (48) String data converted to lower case,
L:307 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:308 M:112 C: (48) String data converted to lower case,

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Input Set : A:\es.txt
Output Set: C:\CRF3\06052001\I701586.raw

L:310 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:311 M:112 C: (48) String data converted to lower case,
L:313 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:314 M:112 C: (48) String data converted to lower case,
L:316 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:317 M:112 C: (48) String data converted to lower case,
L:319 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:320 M:112 C: (48) String data converted to lower case,
L:322 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:323 M:112 C: (48) String data converted to lower case,
L:325 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:326 M:112 C: (48) String data converted to lower case,
L:328 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:329 M:112 C: (48) String data converted to lower case,
L:331 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:332 M:112 C: (48) String data converted to lower case,
L:334 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:335 M:112 C: (48) String data converted to lower case,
L:337 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:338 M:112 C: (48) String data converted to lower case,
L:340 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:341 M:112 C: (48) String data converted to lower case,
L:343 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:344 M:112 C: (48) String data converted to lower case,
L:346 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:347 M:112 C: (48) String data converted to lower case,
L:348 M:112 C: (48) String data converted to lower case,
L:349 M:112 C: (48) String data converted to lower case,
L:350 M:112 C: (48) String data converted to lower case,
L:351 M:112 C: (48) String data converted to lower case,
L:352 M:112 C: (48) String data converted to lower case,
L:353 M:112 C: (48) String data converted to lower case,
L:429 M:342 E: Invalid Stop Code On Error, STOP CODON:
L:444 M:112 C: (48) String data converted to lower case,
L:445 M:112 C: (48) String data converted to lower case,
L:446 M:112 C: (48) String data converted to lower case,
L:447 M:112 C: (48) String data converted to lower case,
L:449 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:450 M:112 C: (48) String data converted to lower case,
L:452 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:453 M:112 C: (48) String data converted to lower case,
L:455 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:456 M:112 C: (48) String data converted to lower case,
L:458 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:459 M:112 C: (48) String data converted to lower case,
L:461 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:462 M:112 C: (48) String data converted to lower case,
L:464 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:465 M:112 C: (48) String data converted to lower case,

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Input Set : A:\es.txt
Output Set: C:\CRF3\06052001\I701586.raw

L:467 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:468 M:112 C: (48) String data converted to lower case,
L:470 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:471 M:112 C: (48) String data converted to lower case,
L:473 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:474 M:112 C: (48) String data converted to lower case,
L:476 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:477 M:112 C: (48) String data converted to lower case,
L:479 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:480 M:112 C: (48) String data converted to lower case,
L:482 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:483 M:112 C: (48) String data converted to lower case,
L:485 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:486 M:112 C: (48) String data converted to lower case,
L:488 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:489 M:112 C: (48) String data converted to lower case,
L:491 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:492 M:112 C: (48) String data converted to lower case,
L:494 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:495 M:112 C: (48) String data converted to lower case,
L:497 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:498 M:112 C: (48) String data converted to lower case,
L:500 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:501 M:112 C: (48) String data converted to lower case,
L:503 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:504 M:112 C: (48) String data converted to lower case,
L:506 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:507 M:112 C: (48) String data converted to lower case,
L:509 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:510 M:112 C: (48) String data converted to lower case,
L:512 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:513 M:112 C: (48) String data converted to lower case,
L:515 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:516 M:112 C: (48) String data converted to lower case,
L:518 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:519 M:112 C: (48) String data converted to lower case,
L:521 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:522 M:112 C: (48) String data converted to lower case,
L:524 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:525 M:112 C: (48) String data converted to lower case,
L:527 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:528 M:112 C: (48) String data converted to lower case,
L:530 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:531 M:112 C: (48) String data converted to lower case,
L:533 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:534 M:112 C: (48) String data converted to lower case,
L:536 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:537 M:112 C: (48) String data converted to lower case,
L:539 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5

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Input Set : A:\es.txt
Output Set: C:\CRF3\06052001\I701586.raw

L:540 M:112 C: (48) String data converted to lower case,
L:542 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:543 M:112 C: (48) String data converted to lower case,
L:545 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:546 M:112 C: (48) String data converted to lower case,
L:548 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:549 M:112 C: (48) String data converted to lower case,
L:551 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:552 M:112 C: (48) String data converted to lower case,
L:553 M:112 C: (48) String data converted to lower case,
L:554 M:112 C: (48) String data converted to lower case,
L:555 M:112 C: (48) String data converted to lower case,
L:556 M:112 C: (48) String data converted to lower case,
L:557 M:112 C: (48) String data converted to lower case,
L:558 M:112 C: (48) String data converted to lower case,
L:634 M:342 E: Invalid Stop Code On Error, STOP CODON:
L:649 M:254 E: No. of Bases conflict, LENGTH:Input:60 Counted:59 SEQ:7
L:649 M:112 C: (48) String data converted to lower case,
L:650 M:254 E: No. of Bases conflict, LENGTH:Input:117 Counted:116 SEQ:7
L:650 M:112 C: (48) String data converted to lower case,
L:653 M:254 E: No. of Bases conflict, LENGTH:Input:165 Counted:164 SEQ:7
L:653 M:112 C: (48) String data converted to lower case,
L:655 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:656 M:254 E: No. of Bases conflict, LENGTH:Input:213 Counted:212 SEQ:7
L:656 M:112 C: (48) String data converted to lower case,
L:658 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:659 M:254 E: No. of Bases conflict, LENGTH:Input:261 Counted:260 SEQ:7
L:659 M:112 C: (48) String data converted to lower case,
L:661 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:662 M:254 E: No. of Bases conflict, LENGTH:Input:309 Counted:308 SEQ:7
L:662 M:112 C: (48) String data converted to lower case,
L:664 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:665 M:254 E: No. of Bases conflict, LENGTH:Input:357 Counted:356 SEQ:7
L:665 M:112 C: (48) String data converted to lower case,
L:667 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:668 M:254 E: No. of Bases conflict, LENGTH:Input:405 Counted:404 SEQ:7
L:668 M:112 C: (48) String data converted to lower case,
L:670 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:671 M:254 E: No. of Bases conflict, LENGTH:Input:453 Counted:452 SEQ:7
L:671 M:112 C: (48) String data converted to lower case,
L:673 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:674 M:254 E: No. of Bases conflict, LENGTH:Input:501 Counted:500 SEQ:7
L:674 M:112 C: (48) String data converted to lower case,
L:676 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:677 M:254 E: No. of Bases conflict, LENGTH:Input:549 Counted:548 SEQ:7
L:677 M:112 C: (48) String data converted to lower case,
L:679 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:680 M:254 E: No. of Bases conflict, LENGTH:Input:597 Counted:596 SEQ:7
L:680 M:112 C: (48) String data converted to lower case,

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Input Set : A:\es.txt
Output Set: C:\CRF3\06052001\I701586.raw

L:682 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:683 M:254 E: No. of Bases conflict, LENGTH:Input:645 Counted:644 SEQ:7
L:683 M:112 C: (48) String data converted to lower case,
L:685 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:686 M:254 E: No. of Bases conflict, LENGTH:Input:693 Counted:692 SEQ:7
L:686 M:112 C: (48) String data converted to lower case,
L:688 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:689 M:254 E: No. of Bases conflict, LENGTH:Input:741 Counted:740 SEQ:7
L:689 M:112 C: (48) String data converted to lower case,
L:691 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:692 M:254 E: No. of Bases conflict, LENGTH:Input:789 Counted:788 SEQ:7
L:692 M:112 C: (48) String data converted to lower case,
L:694 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:695 M:254 E: No. of Bases conflict, LENGTH:Input:837 Counted:836 SEQ:7
L:695 M:112 C: (48) String data converted to lower case,
L:697 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:698 M:254 E: No. of Bases conflict, LENGTH:Input:885 Counted:884 SEQ:7
L:698 M:112 C: (48) String data converted to lower case,
L:700 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:701 M:254 E: No. of Bases conflict, LENGTH:Input:933 Counted:932 SEQ:7
L:701 M:112 C: (48) String data converted to lower case,
L:703 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:704 M:254 E: No. of Bases conflict, LENGTH:Input:981 Counted:980 SEQ:7
L:704 M:112 C: (48) String data converted to lower case,
L:706 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:707 M:254 E: No. of Bases conflict, LENGTH:Input:1029 Counted:1028 SEQ:7
L:707 M:112 C: (48) String data converted to lower case,
L:709 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:710 M:254 E: No. of Bases conflict, LENGTH:Input:1077 Counted:1076 SEQ:7
L:710 M:112 C: (48) String data converted to lower case,
L:712 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:713 M:254 E: No. of Bases conflict, LENGTH:Input:1125 Counted:1124 SEQ:7
L:713 M:112 C: (48) String data converted to lower case,
L:715 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:716 M:254 E: No. of Bases conflict, LENGTH:Input:1173 Counted:1172 SEQ:7
L:716 M:112 C: (48) String data converted to lower case,
L:718 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:719 M:254 E: No. of Bases conflict, LENGTH:Input:1221 Counted:1220 SEQ:7
L:719 M:112 C: (48) String data converted to lower case,
L:721 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:722 M:254 E: No. of Bases conflict, LENGTH:Input:1269 Counted:1268 SEQ:7
L:722 M:112 C: (48) String data converted to lower case,
L:724 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:725 M:254 E: No. of Bases conflict, LENGTH:Input:1317 Counted:1316 SEQ:7
L:725 M:112 C: (48) String data converted to lower case,
L:727 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:728 M:254 E: No. of Bases conflict, LENGTH:Input:1365 Counted:1364 SEQ:7
L:728 M:112 C: (48) String data converted to lower case,
L:730 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7

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DATE: 06/05/2001
TIME: 12:16:02

Input Set : A:\es.txt
Output Set: C:\CRF3\06052001\I701586.raw

L:731 M:254 E: No. of Bases conflict, LENGTH:Input:1413 Counted:1412 SEQ:7
L:731 M:112 C: (48) String data converted to lower case,
L:733 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:734 M:254 E: No. of Bases conflict, LENGTH:Input:1461 Counted:1460 SEQ:7
L:734 M:112 C: (48) String data converted to lower case,
L:736 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:737 M:254 E: No. of Bases conflict, LENGTH:Input:1509 Counted:1508 SEQ:7
L:737 M:112 C: (48) String data converted to lower case,
L:739 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:740 M:254 E: No. of Bases conflict, LENGTH:Input:1557 Counted:1556 SEQ:7
L:740 M:112 C: (48) String data converted to lower case,
L:742 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:743 M:254 E: No. of Bases conflict, LENGTH:Input:1605 Counted:1604 SEQ:7
L:743 M:112 C: (48) String data converted to lower case,
L:745 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:746 M:254 E: No. of Bases conflict, LENGTH:Input:1653 Counted:1652 SEQ:7
L:746 M:112 C: (48) String data converted to lower case,
L:748 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:749 M:254 E: No. of Bases conflict, LENGTH:Input:1701 Counted:1700 SEQ:7
L:749 M:112 C: (48) String data converted to lower case,
L:751 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:752 M:254 E: No. of Bases conflict, LENGTH:Input:1740 Counted:1739 SEQ:7
L:752 M:112 C: (48) String data converted to lower case,
L:753 M:252 E: No. of Seq. differs, <211>LENGTH:Input:1740 Found:1739 SEQ:7
L:843 M:112 C: (48) String data converted to lower case,
L:845 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:846 M:112 C: (48) String data converted to lower case,
L:848 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:849 M:112 C: (48) String data converted to lower case,
L:851 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:852 M:112 C: (48) String data converted to lower case,
L:854 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:855 M:112 C: (48) String data converted to lower case,
L:857 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:858 M:112 C: (48) String data converted to lower case,
L:860 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:861 M:112 C: (48) String data converted to lower case,
L:863 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:864 M:112 C: (48) String data converted to lower case,
L:866 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:867 M:112 C: (48) String data converted to lower case,
L:869 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:870 M:112 C: (48) String data converted to lower case,
L:872 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:873 M:112 C: (48) String data converted to lower case,
L:875 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:876 M:112 C: (48) String data converted to lower case,
L:878 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:879 M:112 C: (48) String data converted to lower case,

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Input Set : A:\es.txt
Output Set: C:\CRF3\06052001\I701586.raw

L:881 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:882 M:112 C: (48) String data converted to lower case,
L:884 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:885 M:112 C: (48) String data converted to lower case,
L:887 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:888 M:112 C: (48) String data converted to lower case,
L:890 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:891 M:112 C: (48) String data converted to lower case,
L:893 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:894 M:112 C: (48) String data converted to lower case,
L:896 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:897 M:112 C: (48) String data converted to lower case,
L:899 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:900 M:112 C: (48) String data converted to lower case,
L:902 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:903 M:112 C: (48) String data converted to lower case,
L:905 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:906 M:112 C: (48) String data converted to lower case,
L:908 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:909 M:112 C: (48) String data converted to lower case,
L:911 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:912 M:112 C: (48) String data converted to lower case,
L:914 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:915 M:112 C: (48) String data converted to lower case,
L:917 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:918 M:112 C: (48) String data converted to lower case,
L:920 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:921 M:112 C: (48) String data converted to lower case,
L:923 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:924 M:112 C: (48) String data converted to lower case,
L:926 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:927 M:112 C: (48) String data converted to lower case,
L:929 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:930 M:112 C: (48) String data converted to lower case,
L:932 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:933 M:112 C: (48) String data converted to lower case,
L:935 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:936 M:112 C: (48) String data converted to lower case,
L:938 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:939 M:112 C: (48) String data converted to lower case,
L:941 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:942 M:112 C: (48) String data converted to lower case,
L:1016 M:252 E: No. of Seq. differs, <211>LENGTH:Input:528 Found:0 SEQ:10
L:1039 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:1070 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:1073 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:1103 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
L:1105 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
L:1108 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13

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Input Set : A:\es.txt
Output Set: C:\CRF3\06052001\I701586.raw

L:1135 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:1138 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:1163 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:1166 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:1188 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16
L:1190 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16
L:1215 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:1217 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:1219 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:1238 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18
L:1256 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:19 differs:18
L:1258 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:0
L:1269 M:250 E: Invalid Numeric Identifier, INVALID IDENTIFIER
L:1270 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:1279 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20
L:1299 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21
L:1302 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21
L:1325 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:1435 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:0
L:1452 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:0
L:1455 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:0
L:1458 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:0
L:1466 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:31 differs:28
L:1480 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:32 differs:28
L:1492 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:33 differs:28
L:20 M:203 E: No. of Seq. differs, <160> Number Of Sequences:Input (33) Counted (31)